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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/898,586

DATE: 09/13/2001
TIME: 12:51:18

Input Set : A:\Cural381.app
Output Set: N:\CRF3\09132001\I898586.raw

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3 <110> APPLICANT: Gerlach, Valerie L
4 MacDougall, John R
5 Smithson, Glenna
7 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
9 <130> FILE REFERENCE: 15966-638CIP
11 <140> CURRENT APPLICATION NUMBER: 09/898,586
C--> 12 <141> CURRENT FILING DATE: 2001-08-27
14 <150> PRIOR APPLICATION NUMBER: 60/177,839
15 <151> PRIOR FILING DATE: 2000-01-25
17 <150> PRIOR APPLICATION NUMBER: 60/176,134
18 <151> PRIOR FILING DATE: 2000-01-14
20 <150> PRIOR APPLICATION NUMBER: 60/175,989
21 <151> PRIOR FILING DATE: 2000-01-13
23 <150> PRIOR APPLICATION NUMBER: 60/218,324
24 <151> PRIOR FILING DATE: 2000-07-14
26 <150> PRIOR APPLICATION NUMBER: 60/220,253
27 <151> PRIOR FILING DATE: 2000-07-24
29 <150> PRIOR APPLICATION NUMBER: 60/178,191
30 <151> PRIOR FILING DATE: 2000-01-26
32 <150> PRIOR APPLICATION NUMBER: 60/178,227
33 <151> PRIOR FILING DATE: 2000-01-26
35 <150> PRIOR APPLICATION NUMBER: 60/220,590
36 <151> PRIOR FILING DATE: 2000-07-25
38 <150> PRIOR APPLICATION NUMBER: 09/761,288
39 <151> PRIOR FILING DATE: 2001-01-16
41 <160> NUMBER OF SEQ ID NOS: 104
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47 <212> TYPE: DNA
48 <213> ORGANISM: Homo sapiens
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53 tcattgcact tttcctgtgt ctctattaa cagggctgtt tggaaactta ctcatcttgc 180
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55 ccttggtaga cctctgcctt ccctcagcca cagccccaa gatgctactg aacatccaaa 300
56 cccaaaccca aaccatctcc tatcccggct gcctggctca gatgtatttgc tgtatgatgt 360
57 ttgccaatat ggacaatttt cttctcacag tggatggcata tgaccgttac gtggccatct 420
58 gtcacccttt acattactcc accattatgg ccctgcgcct ctgtgcctct ctggtagctg 480
59 caccttgggt cattgccatt ttgaaccctc tcttgcacac tcttatgttgc gcccattctgc 540
60 acttctgctc tgataatgtt atccaccatt tcttctgttgc tatcaactct ctcctccctc 600
61 tgtcctgttc cgacaccagt cttaatcagt tggatgttgc ggctacgggt gggctgatct 660
62 ttgtggtacc ttcaagtgtgt atcctggat cctatatcct cattgtttct gctgtgatgt 720
63 aagtcccttc tgcccaagga aaactcaagg ctttctctac ctgtggatct caccttgcct 780
64 tggtcattct tttctatggc gcaatcacag gggctatata gggccctta tccaaatcact 840
65 ctactgaaaa agactcagcc gcatcagtca ttttatggt tggtagcacct gtgttgaatc 900

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 67 gaccgggcgc ggtggctcac gcctgtaatc ccagcactt gggaggccga ggcgggtgga 1020
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 81 20 25 30
 83 Cys Leu Tyr Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala
 84 35 40 45
 86 Ile Gly Ser Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 87 50 55 60
 89 Asn Leu Ser Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys
 90 65 70 75 80
 92 Met Leu Leu Asn Ile Gln Thr Gln Thr Ile Ser Tyr Pro Gly
 93 85 90 95
 95 Cys Leu Ala Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn
 96 100 105 110
 98 Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 99 115 120 125
 101 Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu
 102 130 135 140
 104 Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr
 105 145 150 155 160
 107 Leu Met Met Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His
 108 165 170 175
 110 Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr
 111 180 185 190
 113 Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val
 114 195 200 205
 116 Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala
 117 210 215 220
 119 Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr
 120 225 230 235 240
 122 Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr
 123 245 250 255
 125 Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser
 126 260 265 270
 128 Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
 129 275 280 285
 131 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
 132 290 295 300
 134 Leu Ser Arg Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr Leu
 135 305 310 315 320
 137 Gly Gly Arg Gly Gly Trp Ile Met Arg Ser Gly Asp Arg Asp His Pro

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Input Set : A:\Cural381.app
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152 ctgggatttc ccgttggccc aaggattcag atgctcctct ttgggctctt ctccctgttc 180			
153 tacgtcttca ccctgttggg gaacgggacc atactgggc tcatctcaact ggactccaga 240			
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156 gcgggcccga tggatgcagac ctttctgtt tccacttttgc tggtcacaga atgtctcctc 420			
157 ctgggttgta tgcctatga tctgtacgtg gccatctgcc accccctccg atatttggcc 480			
158 atcatgacctt ggagagtctg catcaccctc gcggtgactt cttggaccac tggagtcctt 540			
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160 tatcaactttttttt tttgtgaaat cttggctgtt ctcaaacttg cctgtgcaga tacccacatc 660			
161 aatgagaaca tggatcttggc cggagcaatt tctggctgg tgggaccctt gtccacaatt 720			
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164 gccattatca tggatgttgg acccagatat gggaaacccca aggagcagaa gaaatatctc 900			
165 ctgctgttca acagcctctt taatccatg ctcaatcccc ttatctgttag tcttaggaac 960			
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180 20 25 30			
182 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile			
183 35 40 45			
185 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His			
186 50 55 60			
188 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met			
189 65 70 75 80			
191 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg			
192 85 90 95			
194 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu			
195 100 105 110			
197 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro			
198 115 120 125			
200 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala			
201 130 135 140			
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207				165			170									175
209	Phe	Cys	Glu	Ile	Leu	Ala	Val	Leu	Lys	Leu	Ala	Cys	Ala	Asp	Thr	His
210				180			185								190	
212	Ile	Asn	Glu	Asn	Met	Val	Leu	Ala	Gly	Ala	Ile	Ser	Gly	Leu	Val	Gly
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215	Pro	Leu	Ser	Thr	Ile	Val	Val	Ser	Tyr	Met	Cys	Ile	Leu	Cys	Ala	Ile
216		210			215		220									
218	Leu	Gln	Ile	Gln	Ser	Arg	Glu	Val	Gln	Arg	Lys	Ala	Phe	Arg	Thr	Cys
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221	Phe	Ser	His	Leu	Cys	Val	Ile	Gly	Leu	Val	Tyr	Gly	Thr	Ala	Ile	Ile
222			245		250		255									
224	Met	Tyr	Val	Gly	Pro	Arg	Tyr	Gly	Asn	Pro	Lys	Glu	Gln	Lys	Lys	Tyr
225		260		265		270										
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244	tgg	ttt	tct	cag	cct	gggg	gag	ctc	cag	tgc	tgc	tct	ttt	ttt	ttt	ttt
245	act	tg	aca	at	c	ctg	gt	gg	gg	ctt	tc	tat	ttt	ttt	ttt	ttt
246	tcc	ac	act	cc	ca	tat	gg	gc	cc	tat	ttt	ttt	ttt	ttt	ttt	ttt
247	ttg	t	tc	at	tc	at	tc	ttt								
248	ttg	c	c	c	c	c	c	cc								
249	ttg	c	c	c	c	c	c	cc								
250	tc	at	aa	ac	aa	aa	gg	gt	gg	tt	tc	tc	tc	tc	tc	tc
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260	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt
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 274 20 25 30
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 277 35 40 45
 279 Val Ile Arg Phe Ser Trp Thr Leu His Thr Pro Met Tyr Gly Phe Leu
 280 50 55 60
 282 Phe Ile Leu Ser Phe Ser Glu Ser Cys Tyr Thr Phe Val Ile Ile Pro
 283 65 70 75 80
 285 Gln Leu Leu Val His Leu Leu Ser Asp Thr Lys Thr Ile Ser Phe Met
 286 85 90 95
 288 Ala Cys Ala Thr Gln Leu Phe Phe Phe Leu Gly Phe Ala Cys Thr Asn
 289 100 105 110
 291 Cys Leu Leu Ile Ala Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
 292 115 120 125
 294 His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
 295 130 135 140
 297 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
 298 145 150 155 160
 300 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
 301 165 170 175
 303 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
 304 180 185 190
 306 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
 307 195 200 205
 309 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
 310 210 215 220
 312 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
 313 225 230 235 240
 315 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
 316 245 250 255
 318 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
 319 260 265 270
 321 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
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 333 <212> TYPE: DNA
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 339 acttgacaat cctggtgccc aatgtgacca tcatggccgt tattcgcttc agctggactc 180

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
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L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:2209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:2749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:2752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63